CLAIMS

1. (Amended) A method of modifying the content and/or composition of one or more metabolites in the storage organs of a plant, said method at least comprising the step of expressing in the storage organ of said plant a chimeric gene that comprises a genetic sequence encoding a sulfur-rich protein placed operably in connection with a promoter capable of conferring expression on said gene in the storage organ of said plant, subject to the proviso that the modified metabolites do not consist of only the sulfurous protein content of a seed and/or wherein the content of an amino acid is modified, such modification is not the result of the presence of a naturally or artificially high level of that amino acid in the sulfur-rich protein.

2. The method according to claim 1 wherein the storage organ is a seed.

3. The method according to ~~claims 1 or 2~~ wherein the metabolite(s) is(are) selected from the list comprising amino acids (either free or incorporated into protein), oils (i.e. fatty acids), protein, sulfurous protein, non-sulfurous protein, starch, soluble and/or insoluble non-starch polysaccharide (NSP), fibre and endogenous anti-nutritional factors.

4. The method according to ~~claims 2 or~~ 3 wherein the total protein content of seeds and/or the starch content of seeds and/or the fatty acid content of seeds and/or the fatty acid composition of seeds and/or the fibre content of seeds and/or the fibre quality of seeds and/or the content of endogenous anti-nutritional factors in seeds is modified.

5. The method according to claim 4 wherein the total protein content is increased.

6. The method according to claim 4 wherein the total fibre content is increased or decreased.

7. The method according to claim 4 wherein the content of endogenous anti-nutritional factors is decreased.

8. The method according to claim 4 wherein the fatty acid content is increased or decreased.

9. The method according to ~~claims 4 or 7~~ wherein the anti-nutritional factor is a protease inhibitor.

10. The method according to claim 9 wherein the protease inhibitor is trypsin inhibitor

and/or chymotrypsin inhibitor.

11. The method according to any one of ~~claims~~ 1 ~~to 10~~ wherein the sulfur-rich protein comprises an amino acid sequence that is rich in methionine and/or cysteine.

12. The method according to claim 11 wherein the sulfur-rich protein is sunflower seed albumin (SSA).

13. The method according to claim 11 wherein the sulfur-rich protein is a 2S protein or the Asp1 synthetic protein.

14. The method according to ~~any one of claims~~ 1 ~~to 13~~ wherein the plant is a dicotyledonous plant.

15. The method according to claim 14 wherein the dicotyledonous plant is a pea, chickpea or lupin plant.

16. The method according to ~~claims~~ 14 ~~or 15~~ wherein the promoter comprises the pea vicilin gene promoter sequence.

17. The method according to ~~any one of claims~~ 1 ~~to 13~~ wherein the plant is a monocotyledonous plant.

18. The method according to claim 17 wherein the monocotyledonous plant is a rice plant.

19. The method according to ~~claims~~ 17 ~~or 18~~ wherein the promoter comprises a *Triticum aestivum* HMW glutenin promoter sequence such as the Bx17 promoter sequence or the JAN808 promoter sequence.

20. The method according to ~~any one of claims~~ 1 ~~to 19~~ further comprising the first steps of:

(i) introducing the chimeric gene into a plant cell, tissue, organ or whole organism; and

(ii) regenerating an intact plant therefrom.

21. A method of increasing the protein content of seeds of a plant, said method at least

comprising the step of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant, subject to the proviso that the sulfurous protein content of the seed alone is not increased.

22. The method according to claim 21 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

23. The method according to claim 21 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

24. The method according to ~~claims~~ Claim 22 ~~or 23~~ wherein the plant is pea or chickpea.

25. The method according to claim 21 wherein the promoter sequence is a wheat HMW glutenin gene promoter and the plant is a monocotyledonous plant.

26. The method according to claim 21 wherein the chimeric gene further comprises the wheat HMW glutenin gene promoter and/or NOS transcription terminator sequences.

27. The method according to ~~claims~~ Claim 25 ~~or 26~~ wherein the plant is a rice plant.

28. A method of modifying the fatty acid content of seeds of a plant, said method at least comprising the step of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant.

29. The method according to claim 28 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

30. The method according to claim 28 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

31. The method according to ~~claims~~ Claim 29 ~~or 30~~ wherein if the plant is lupin the level of fatty acids in the seeds is increased.

32. The method according to ~~claims~~ claim 29 ~~or 30~~ wherein if the plant is pea the level of fatty acids in the seeds is decreased.

33. A method of modifying the fatty acid composition of seeds of a plant, said method at least comprising the step of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant.

34. The method according to claim 33 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

35. The method according to claim 33 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

36. The method according to ~~claims~~ claim 34 ~~or 35~~ wherein the plant is lupin.

37. The method according to ~~any one of claims~~ claim 33 ~~to 36~~ wherein content of myristic acid and/or stearic acid and/or gadoleic acid and/or behenic acid and/or lignoceric acid and/or oleic acid and/or linoleic acid and/or linolenic acid and/or erucic acid is modified.

38. A method of decreasing the starch content of seeds of a plant, said method at least comprising the step of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant.

39. The method according to claim 38 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

40. The method according to claim 38 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

41. The method according to ~~claims~~ claim 39 ~~or 40~~ wherein the plant is a pea plant.

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42. (Amended) A method of modifying the amino acid composition of seeds of a plant, said method at least comprising the step of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant, subject to the proviso that the modified composition of any amino acid is not the result of the presence of a naturally or artificially high level of that amino acid in a sulfur-rich protein.

43. The method according to claim 42 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

44. The method according to claim 42 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

a 45. The method according to ~~claims~~ claim 43 ~~or 44~~ wherein the plant is pea or chickpea.

46. The method according to claim 45 wherein the proportion of arginine relative to other amino acids is increased.

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47. A method of modifying the fibre content of seeds of a plant, said method at least comprising the step of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant.

48. The method according to claim 47 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

49. The method according to claim 47 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

a 50. The method according to ~~claims~~ claim 48 ~~or 49~~ wherein if the plant is lupin the level of soluble fibre including soluble NSP in the seed is decreased.

a 51. The method according to ~~claims~~ claim 48 ~~or 49~~ wherein if the plant is a pea plant the level of fibre in the seed is increased.

52. A method of modifying the fibre quality of seeds of a plant, said method at least comprising the step of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant.

53. The method according to claim 52 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

54. The method according to claim 53 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

55. The method according to ~~claims~~ claim 53 ~~or 54~~ wherein the plant is lupin.

56. The method according to ~~any one of claims~~ claim 52 ~~to 55~~ wherein the soluble NSP content and/or the insoluble NSP content of the seed is decreased.

57. The method according to ~~any one of claims~~ claim 52 ~~to 56~~ wherein the lignin content of the seed is increased.

58. A method of decreasing the endogenous anti-nutritional factor content of seeds of a plant, said method at least comprising the step of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant.

59. The method according to claim 58 wherein the anti-nutritional factor is a sulfur-rich protease inhibitor and/or soluble NSP.

60. The method according to claim 59 wherein the sulfur-rich protease inhibitor is trypsin inhibitor and/or chymotrypsin inhibitor.

61. The method according to any one of ~~claims~~ claim 58 ~~to 60~~ wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

62. The method according to any one of ~~claims~~ claim 58 ~~to 60~~ wherein the chimeric gene further

comprises the pea vicilin gene promoter and transcription terminator sequences.

63. The method according to ~~claims~~ claim 61 ~~or 62~~ wherein the plant is lupin, pea or chickpea.

64. The method according to any one of claims 21 to 63 further comprising the first steps of:

(i) introducing the chimeric gene into a plant cell, tissue, organ or whole organism; and

(ii) regenerating an intact plant therefrom.

65. A transformed plant produced by the method according to any one of claims 1 to 64.

66. Progeny derived from the plant according to claim 65, wherein said progeny comprises at least one copy of the chimeric gene present in the plant according to claim 65 in an expressible format.

67. A plant part derived from the plant according to claim 65 or the progeny according to claim 64 wherein said plant part comprises at least one copy of the chimeric gene present in said plant or progeny in an expressible format.

68. The plant part according to claim 67 comprising leaves, stems, roots, shoots, seed, tubers or flowers.

69. The plant part according to claim 67 comprising seeds.

70. Use of a structural gene sequence that encodes sunflower seed albumin (SSA) to produce a genetic construct which when expressed in the seeds of a plant increases the total protein content of the seed, subject to the proviso that expression of the genetic construct does not only increase the sulfurous protein content of the seed.

71. Use of a structural gene sequence that encodes sunflower seed albumin (SSA) to produce a genetic construct which when expressed in the seeds of a plant modifies the amino acid composition of the seed, subject to the proviso that expression of the genetic construct does not only increase the sulfur-containing amino acid content of the seed.

72. Use of a structural gene sequence that encodes sunflower seed albumin (SSA) to

produce a genetic construct which when expressed in the seeds of a plant increases or decreases the fibre content of the seed.

73. Use of a structural gene sequence that encodes sunflower seed albumin (SSA) to produce a genetic construct which when expressed in the seeds of a plant modifies the fibre composition of the seed.

74. Use of a structural gene sequence that encodes sunflower seed albumin (SSA) to produce a genetic construct which when expressed in the seeds of a plant decreases the total starch content of the seed.

75. Use of a structural gene sequence that encodes sunflower seed albumin (SSA) to produce a genetic construct which when expressed in the seeds of a plant increases or decreases the total fatty acid content of the seed.

76. Use of a structural gene sequence that encodes sunflower seed albumin (SSA) to produce a genetic construct which when expressed in the seeds of a plant modifies the fatty acid composition of the seed.

77. Use of a structural gene sequence that encodes sunflower seed albumin (SSA) to produce a genetic construct which when expressed in the seeds of a plant decreases the anti-nutritional factor content of the seed.

78. Use according to any one of claims 70 to 77 wherein the genetic construct further comprises a promoter sequence which confers strong expression at least in the seeds of the plant.

79. Use according to claim 78 wherein the promoter is the pea vicilin gene promoter.

80. Use according to claim 78 wherein the promoter is the wheat HMW glutenin gene promoter.

81. Use according to any one of claims 70 to 80 wherein the genetic construct further comprises a transcription terminator sequence placed downstream of the coding region of the structural gene sequence.

82. Use according to claim 81 wherein the transcription terminator sequence is the pea vicilin gene terminator sequence.

83. Use of the transformed plant according to claim 65 to produce a food composition for consumption by humans or animals.

84. Use of the progeny plant according to claim ~~66~~ 65 to produce a food composition for consumption by humans or animals.

85. Use of the plant part according to ~~any one of claims~~ 67 ~~to 69~~ to produce a food composition for consumption by humans or animals.

86. The method according to any one of claims 1, 21, 38, 42, 47, 52 or 58, wherein the storage organ is a tuber.

87. The method according to any one of claims 1, 21, 38, 42, 47, 52 or 58, wherein the storage organ is a specialised stem.